IFWO

RAW SEQUENCE LISTING   DATE: 10/12/2004
PATENT APPLICATION: US/10/763,976A   TIME: 12:30:42

Input Set : **D:\Warf Sequence.ST25.txt**
Output Set: **N:\CRF4\10122004\J763976A.raw**

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 3 <110> APPLICANT: Harms, Jerome S
 4         Splitter, Gary A
 5         Eakle, Kurt A
 6         Bremel, Robert D
 8 <120> TITLE OF INVENTION: Inducible Protein Expression System
10 <130> FILE REFERENCE: 2240/3
12 <140> CURRENT APPLICATION NUMBER: US 10/763,976A
13 <141> CURRENT FILING DATE: 2004-01-23
15 <160> NUMBER OF SEQ ID NOS: 65
17 <170> SOFTWARE: PatentIn version 3.3
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 576
21 <212> TYPE: DNA
22 <213> ORGANISM: Artificial
24 <220> FEATURE:
25 <223> OTHER INFORMATION: Engineered Sequence from virus and plasmid
28 <220> FEATURE:
29 <221> NAME/KEY: Promoter
30 <222> LOCATION: (87)..(432)
31 <223> OTHER INFORMATION: BLV Promoter
33 <400> SEQUENCE: 1
34 aggaaaccag cagcggctat ccgcgcatcc atgcccccga actgcaggag tggggaggca     60
36 cgatggccgc tttggtcgag gcggatccta gcagaaaaat aagacttgat tcccccttaa    120
38 aattacaact gctagaaaat gaatggctct cccgcctttt ttgaggggga atcatttgta    180
40 tgaaagatca tgccgaccta ggcgccgcca ccgccccgta aaccagacag agacgtcagc    240
42 tgccagaaaa gctggtgacg gcagctggtg gctagaatcc ccgtacctcc ccaacttccc    300
44 ctttcccgaa aaatccacac cctgagctgc tgacctcacc tgctgataaa ttaataaaat    360
46 gccggccctg tcgagttagc ggcaccagaa gcgttcttct cctgagaccc tcgtgctcag    420
48 ctctcggtcc tgcctcgaga agcttgttat cacaagtttg tacaaaaaag ctgaacgaga    480
50 aacgtaaaat gatataaata tcaatatatt aaattagatt ttgcataaaa aacagactac    540
52 ataatactgt aaaacacaac atatccagtc actatg                             576
55 <210> SEQ ID NO: 2
56 <211> LENGTH: 930
57 <212> TYPE: DNA
58 <213> ORGANISM: Bovine leukemia virus
61 <220> FEATURE:
62 <221> NAME/KEY: CDS
63 <222> LOCATION: (1)..(930)
65 <400> SEQUENCE: 2
66 atg gca agt gtt gtt ggt tgg ggg ccc cac tct cta cat gcc tgc ccg      48
67 Met Ala Ser Val Val Gly Trp Gly Pro His Ser Leu His Ala Cys Pro
68 1               5                   10                  15
70 gcc ctg gtt ttg tcc aat gac gtc acc atc gat gcc tgg tgc ccc ctc      96
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 71 Ala Leu Val Leu Ser Asn Asp Val Thr Ile Asp Ala Trp Cys Pro Leu
 72             20                  25                  30
 74 tgc ggg ccc cat gag cga ctc caa ttc gaa agg atc gac acc acg cac    144
 75 Cys Gly Pro His Glu Arg Leu Gln Phe Glu Arg Ile Asp Thr Thr His
 76         35                  40                  45
 78 acc tgc gag acc cac cgt atc acc tgg acc gcc gat gga cga cct ttc    192
 79 Thr Cys Glu Thr His Arg Ile Thr Trp Thr Ala Asp Gly Arg Pro Phe
 80         50                  55                  60
 82 ggc ctc aat gga gcg ctg ttc cct cga ctg cat gtc tcc aga gac ccg    240
 83 Gly Leu Asn Gly Ala Leu Phe Pro Arg Leu His Val Ser Arg Asp Pro
 84 65                  70                  75                  80
 86 gcc cca agg gcc cga cga ctc tgg atc aac tgc ccc ctt ccg gcc gtt    288
 87 Ala Pro Arg Ala Arg Arg Leu Trp Ile Asn Cys Pro Leu Pro Ala Val
 88                 85                  90                  95
 90 cgc gct cag ccc ggc ccg gtt tca ctt tcc ccc ttc gag cgg tcc ccc    336
 91 Arg Ala Gln Pro Gly Pro Val Ser Leu Ser Pro Phe Glu Arg Ser Pro
 92             100                 105                 110
 94 ttc cag ccc tac caa tgc caa ttg ccc tcg gcc tct agc gac ggt tgc    384
 95 Phe Gln Pro Tyr Gln Cys Gln Leu Pro Ser Ala Ser Ser Asp Gly Cys
 96         115                 120                 125
 98 ccc gtc atc ggg cac ggc ctt ctt ccc tgg aac aac tta gta acg cat    432
 99 Pro Val Ile Gly His Gly Leu Leu Pro Trp Asn Asn Leu Val Thr His
100         130                 135                 140
102 cct tgt cct cgg aaa gtc ctt ata tta aat caa atg gcc aat ttt tcc    480
103 Pro Cys Pro Arg Lys Val Leu Ile Leu Asn Gln Met Ala Asn Phe Ser
104 145                 . 150                 155                 160
106 tta ctc ccc ccc ttc aat acc ctc ctt gtg gac ccc ctc cgg ttg tcc    528
107 Leu Leu Pro Pro Phe Asn Thr Leu Leu Val Asp Pro Leu Arg Leu Ser
108                 165                 170                 175
110 gtc ttt gcc cca gac acc agg gga gcc ata cgt tat ctc tcc acc ctt    576
111 Val Phe Ala Pro Asp Thr Arg Gly Ala Ile Arg Tyr Leu Ser Thr Leu
112             180                 185                 190
114 ttg acg cta tgc cca gct act tgt att cta ccc ctc ggc gag ccc ttc    624
115 Leu Thr Leu Cys Pro Ala Thr Cys Ile Leu Pro Leu Gly Glu Pro Phe
116         195                 200                 205
118 tct cct aat gtc ccc ata tgt cgc ttt ccc cgg gac tcc aat gaa ccc    672
119 Ser Pro Asn Val Pro Ile Cys Arg Phe Pro Arg Asp Ser Asn Glu Pro
120         210                 215                 220
122 ccc ctt tca gaa ttc gag ctg ccc ctt atc caa acg ccc ggc ctg tct    720
123 Pro Leu Ser Glu Phe Glu Leu Pro Leu Ile Gln Thr Pro Gly Leu Ser
124 225                 230                 235                 240
126 tgg tct gtc ccc gcg atc gac cta ttc cta acc ggc ccc cct tcc cca    768
127 Trp Ser Val Pro Ala Ile Asp Leu Phe Leu Thr Gly Pro Pro Ser Pro
128                 245                 250                 255
130 tgc gac cgg tta cac gta tgg tcc agt cct cag gcc tta cag cgc ttc    816
131 Cys Asp Arg Leu His Val Trp Ser Ser Pro Gln Ala Leu Gln Arg Phe
132         260                 265                 270
134 ctc cat gac cct acg cta acc tgg tca gaa ttg gtt gct agc agg aaa    864
135 Leu His Asp Pro Thr Leu Thr Trp Ser Glu Leu Val Ala Ser Arg Lys
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136          275                280                285
138 cta aga ctt gat tca ccc tta aaa tta caa ctg tta gaa aat gaa tgg      912
139 Leu Arg Leu Asp Ser Pro Leu Lys Leu Gln Leu Leu Glu Asn Glu Trp
140      290                295                300
142 ctc tcc cgc ctt ttt tga                                               930
143 Leu Ser Arg Leu Phe
144 305

147 <210> SEQ ID NO: 3
148 <211> LENGTH: 309
149 <212> TYPE: PRT
150 <213> ORGANISM: Bovine leukemia virus

152 <400> SEQUENCE: 3

154 Met Ala Ser Val Val Gly Trp Gly Pro His Ser Leu His Ala Cys Pro
155 1               5                   10                  15
158 Ala Leu Val Leu Ser Asn Asp Val Thr Ile Asp Ala Trp Cys Pro Leu
159          20                  25                  30
162 Cys Gly Pro His Glu Arg Leu Gln Phe Glu Arg Ile Asp Thr Thr His
163          35                  40                  45
166 Thr Cys Glu Thr His Arg Ile Thr Trp Thr Ala Asp Gly Arg Pro Phe
167      50                  55                  60
170 Gly Leu Asn Gly Ala Leu Phe Pro Arg Leu His Val Ser Arg Asp Pro
171 65                  70                  75                  80
174 Ala Pro Arg Ala Arg Arg Leu Trp Ile Asn Cys Pro Leu Pro Ala Val
175              85                  90                  95
178 Arg Ala Gln Pro Gly Pro Val Ser Leu Ser Pro Phe Glu Arg Ser Pro
179              100                 105                 110
182 Phe Gln Pro Tyr Gln Cys Gln Leu Pro Ser Ala Ser Ser Asp Gly Cys
183          115                 120                 125
186 Pro Val Ile Gly His Gly Leu Leu Pro Trp Asn Asn Leu Val Thr His
187      130                 135                 140
190 Pro Cys Pro Arg Lys Val Leu Ile Leu Asn Gln Met Ala Asn Phe Ser
191 145              150                 155                 160
194 Leu Leu Pro Pro Phe Asn Thr Leu Leu Val Asp Pro Leu Arg Leu Ser
195              165                 170                 175
198 Val Phe Ala Pro Asp Thr Arg Gly Ala Ile Arg Tyr Leu Ser Thr Leu
199              180                 185                 190
202 Leu Thr Leu Cys Pro Ala Thr Cys Ile Leu Pro Leu Gly Glu Pro Phe
203          195                 200                 205
206 Ser Pro Asn Val Pro Ile Cys Arg Phe Pro Arg Asp Ser Asn Glu Pro
207      210                 215                 220
210 Pro Leu Ser Glu Phe Glu Leu Pro Leu Ile Gln Thr Pro Gly Leu Ser
211 225              230                 235                 240
214 Trp Ser Val Pro Ala Ile Asp Leu Phe Leu Thr Gly Pro Pro Ser Pro
215              245                 250                 255
218 Cys Asp Arg Leu His Val Trp Ser Ser Pro Gln Ala Leu Gln Arg Phe
219          260                 265                 270
222 Leu His Asp Pro Thr Leu Thr Trp Ser Glu Leu Val Ala Ser Arg Lys
223      275                 280                 285
226 Leu Arg Leu Asp Ser Pro Leu Lys Leu Gln Leu Leu Glu Asn Glu Trp
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```
227     290                 295                 300
230 Leu Ser Arg Leu Phe
231 305
234 <210> SEQ ID NO: 4
235 <211> LENGTH: 1062
236 <212> TYPE: DNA
237 <213> ORGANISM: Human T-cell lymphotropic virus type 1
240 <220> FEATURE:
241 <221> NAME/KEY: promoter
242 <222> LOCATION: (1)..(353)
244 <400> SEQUENCE: 4
245 atggcccact tcccagggtt tggacagagt cttcttttcg gatacccagt ctacgtgttt      60
247 ggagacggcg actggtgccc ctgtgtacaa atctctgggg gactatgttc ggcccgccta     120
249 catcgtcacg ccctactggc cacctgtcca gagcatcaga tcacctggga ccccatcgat     180
251 ggacgcgtta tcggctcagc tctacagttc cttatccctc gactcccctc cttccccacc     240
253 cagagaacct ctaagaccct caaggtcctt accccgccaa tcactcatac aaccccccaac    300
255 attccaccct ccttcctcca ggccatgcgc aaatactccc ccttccgaaa tggatacatg     360
257 gaacccaccc ttgggcagca cctcccaacc ctgtcttttc cagaccccgg actccggccc     420
259 caaaacctgt acaccctctg gggaggctcc gttgtctgca tgtacctcta ccagctttcc     480
261 ccccccatca cctggcccct cctgccccac gtgattttt gccacccgg ccagctcggg       540
263 gccttcctca ccaatgttcc ctacaagcga atagaagaac tcctctataa aatttccctt     600
265 accacagggg ccctaataat tctacccgaa gactgtttgc ccaccacct tttccagcct      660
267 gttagggcac ccgtcacgct aacagcctgg caaaacggcc tccttccgtt ccactcaacc     720
269 ctcaccactc caggccttat ttggacattt accgatggca cgcctatgat ttccgggccc     780
271 tgccctaaag atggccagcc atctttagta ctacagtcct cctcctttat atttcacaaa     840
273 tttcaaacca aggcctacca cccctcattt ctactctcac acggcctcat acagtactct     900
275 tcctttcata atttacatct cctgtttgaa gaatacacca acatccccat ttctctactt     960
277 tttaacaaaa aagaggcaga tgacaatgac catgagcccc aaatatcccc cggggggctta   1020
279 gagcctccca gtgaaaaaca tttccgcgaa acagaagtct ga                        1062
282 <210> SEQ ID NO: 5
283 <211> LENGTH: 353
284 <212> TYPE: DNA
285 <213> ORGANISM: Human T-cell lymphotropic virus type 1
287 <400> SEQUENCE: 5
288 tgacaatgac catgagcccc aaatatcccc cggggggctta gagcctctca gtgaaaaaca     60
290 tttccgtgaa acagaagtct gagaaggtca gggcccagaa taaggctctg acgtctcccc     120
292 ccggaggaca gctcagcacc agctcaggct aggccctgac gtgtcccccт aaagacaaat     180
294 cataagctca gacctccggg aagccaccgg gaaccaccca tttcctcccc atgtttgtca     240
296 agccgtcctc aggcgttgac gacaaccccт cacctcaaaa aacttttcat ggcacgcata     300
298 cggctcaata aaataacagg agtctataaa agcgtgggga cagttcagga ggg             353
301 <210> SEQ ID NO: 6
302 <211> LENGTH: 456
303 <212> TYPE: DNA
304 <213> ORGANISM: Human immunodeficiency virus type 1
307 <220> FEATURE:
308 <221> NAME/KEY: CDS
309 <222> LOCATION: (1)..(456)
311 <400> SEQUENCE: 6
312 ctg gaa ggg cta att tgg tcc caa aga aga caa gag atc ctt gat ctg         48
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Input Set : **D:\Warf Sequence.ST25.txt**
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313 Leu Glu Gly Leu Ile Trp Ser Gln Arg Arg Gln Glu Ile Leu Asp Leu
314 1               5                   10                  15
316 tgg atc tac cac aca caa ggc tac ttc cct gat tgg cag aat tac aca       96
317 Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr
318             20                  25                  30
320 cca ggg cca ggg atc aga tat cca ctg acc ttt gga tgg tgc ttc aag      144
321 Pro Gly Pro Gly Ile Arg Tyr Pro Leu Thr Phe Gly Trp Cys Phe Lys
322         35                  40                  45
324 cta gta cca gtt gag cca gag aag gta gaa gag gcc aat gaa gga gag      192
325 Leu Val Pro Val Glu Pro Glu Lys Val Glu Glu Ala Asn Glu Gly Glu
326     50                  55                  60
328 aac aac agc ttg tta cac cct atg agc ctg cat ggg atg gag gac gcg      240
329 Asn Asn Ser Leu Leu His Pro Met Ser Leu His Gly Met Glu Asp Ala
330 65                  70                  75                  80
332 gag aaa gaa gtg tta gtg tgg agg ttt gac agc aaa cta gca ttt cat      288
333 Glu Lys Glu Val Leu Val Trp Arg Phe Asp Ser Lys Leu Ala Phe His
334                 85                  90                  95
336 cac atg gcc cga gag ctg cat ccg gag tac tac aaa gac tgc tga cat      336
337 His Met Ala Arg Glu Leu His Pro Glu Tyr Tyr Lys Asp Cys     His
338             100                 105                 110
340 cga gct ttc tac aag gga ctt tcc gct ggg gac ttt cca ggg agg cgt      384
341 Arg Ala Phe Tyr Lys Gly Leu Ser Ala Gly Asp Phe Pro Gly Arg Arg
342             115                 120                 125
344 ggc ctg ggc ggg act ggg gag tgg cgt ccc tca gat gct gca tat aag      432
345 Gly Leu Gly Gly Thr Gly Glu Trp Arg Pro Ser Asp Ala Ala Tyr Lys
346         130                 135                 140
348 cag ctg ctt ttt gcc tgt act ggg                                     456
349 Gln Leu Leu Phe Ala Cys Thr Gly
350     145                 150
353 <210> SEQ ID NO: 7
354 <211> LENGTH: 110
355 <212> TYPE: PRT
356 <213> ORGANISM: Human immunodeficiency virus type 1
358 <400> SEQUENCE: 7
360 Leu Glu Gly Leu Ile Trp Ser Gln Arg Arg Gln Glu Ile Leu Asp Leu
361 1               5                   10                  15
364 Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr
365             20                  25                  30
368 Pro Gly Pro Gly Ile Arg Tyr Pro Leu Thr Phe Gly Trp Cys Phe Lys
369         35                  40                  45
372 Leu Val Pro Val Glu Pro Glu Lys Val Glu Glu Ala Asn Glu Gly Glu
373     50                  55                  60
376 Asn Asn Ser Leu Leu His Pro Met Ser Leu His Gly Met Glu Asp Ala
377 65                  70                  75                  80
380 Glu Lys Glu Val Leu Val Trp Arg Phe Asp Ser Lys Leu Ala Phe His
381                 85                  90                  95
384 His Met Ala Arg Glu Leu His Pro Glu Tyr Tyr Lys Asp Cys
385             100                 105                 110
388 <210> SEQ ID NO: 8
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 10/12/2004
PATENT APPLICATION: **US/10/763,976A**   TIME: 12:30:43

Input Set : **D:\Warf Sequence.ST25.txt**
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Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37
Seq#:38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61
Seq#:62,63,64,65

VERIFICATION SUMMARY   DATE: 10/12/2004
PATENT APPLICATION: **US/10/763,976A**   TIME: 12:30:43

Input Set : **D:\Warf Sequence.ST25.txt**
Output Set: **N:\CRF4\10122004\J763976A.raw**